

L Number	Hits	Search Text	DB	Time stamp
1	2	communi-d.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/23 15:03
2	1	pirotton-sabine.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/23 15:03
3	14	parmentier-marc.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/23 15:03
4	5	boeynaems-jean-marie.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/23 15:04
5	100	uridine same receptor same protein	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/23 15:04
6	3111	uridine and receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/23 15:05
7	0	uridine adj receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/23 15:05
8	29	(purinergic adj receptor) same uridine	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/23 15:05

## Sequence Comparison A

### RESULT 1

#### P2Y4\_HUMAN

ID P2Y4\_HUMAN STANDARD; PRT; 365 AA.

AC P51582;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE P2Y purinoceptor 4 (P2Y4) (Uridine nucleotide receptor) (UNR) (P2P).

GN P2RY4 OR NRU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96125055; PubMed=8537336;

RA Communi D., Pirotton S., Parmentier M., Boeynaems J.-M.;

RT "Cloning and functional expression of a human uridine nucleotide

RT receptor.";

RL J. Biol. Chem. 270:30849-30852(1995).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=96125054; PubMed=8537335;

RA Nguyen T., Erb L., Weisman G.A., Marchese A., Heng H.H.Q.,

RA Garrad R.C., George S.R., Turner J.T., O'Dowd B.F.;

RT "Cloning, expression, and chromosomal localization of the human

RT uridine nucleotide receptor gene.";

RL J. Biol. Chem. 270:30845-30848(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RX MEDLINE=96197801; PubMed=8617367;

RA Stam N.J., Klomp J., van der Heuvel M., Olijve W.;

RT "Molecular cloning and characterization of a novel orphan receptor

RT (P2P) expressed in human pancreas that shows high structural homology

RT to the P2U purinoceptor.";

RL FEBS Lett. 384:260-264(1996).

CC -!- FUNCTION: Receptor for UTP and UDP coupled to G-proteins that

CC activate a phosphatidylinositol-calcium second messenger system.

CC Not activated by ATP or ADP.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Pancreas.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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DR EMBL; X91852; CAA62963.1; -.

DR EMBL; U40223; AAC50347.1; -.

DR EMBL; X96597; CAA65415.1; -.

DR HSSP; P34996; 1DDD.

DR Genew; HGNC:8542; P2RY4.

DR MIM; 300038; -.

DR InterPro; IPR000276; GPCR\_Rhodpsn.

DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Polymorphism.

FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 61 1 (POTENTIAL).

FT DOMAIN 62 72 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	73	95	2 (POTENTIAL).
FT	DOMAIN	96	112	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	113	131	3 (POTENTIAL).
FT	DOMAIN	132	154	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	155	174	4 (POTENTIAL).
FT	DOMAIN	175	196	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	197	222	5 (POTENTIAL).
FT	DOMAIN	223	246	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	247	269	6 (POTENTIAL).
FT	DOMAIN	270	287	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	288	309	7 (POTENTIAL).
FT	DOMAIN	310	365	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	108	185	BY SIMILARITY.
FT	VARIANT	168	168	V -> M (IN DBSNP:1152186).
FT				/FTId=VAR_011854.
FT	VARIANT	178	178	N -> T (IN DBSNP:1152187).
FT				/FTId=VAR_011855.
FT	VARIANT	191	191	P -> L (IN DBSNP:1152188).
FT				/FTId=VAR_011856.
FT	CONFLICT	86	86	L -> V (IN REF. 2).
FT	CONFLICT	234	234	S -> A (IN REF. 2).
SQ	SEQUENCE	365 AA;	40963 MW;	23E0AFED3B7BDEED CRC64;

Query Match 100.0%; Score 1944; DB 1; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
 Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKILLPVSYAVVFVLGLGLNAPTLWLF	60
Db	1	MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKILLPVSYAVVFVLGLGLNAPTLWLF	60
Qy	61	IFRLRPWDATATYMFHLALSDTLYVLSLPTLIYYAAHNHWPFGEICKFVRFLFYWNLY	120
Db	61	IFRLRPWDATATYMFHLALSDTLYVLSLPTLIYYAAHNHWPFGEICKFVRFLFYWNLY	120
Qy	121	CSVLF LTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVWL VVAGCLVPNLFFVTTSNKG	180
Db	121	CSVLF LTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVWL VVAGCLVPNLFFVTTSNKG	180
Qy	181	TTVLCHD TTRPEEFDHYVHFSSAVMGLLFGVPCLVTLVCYGLMARRLYQPLPGSAQSSSR	240
Db	181	TTVLCHD TTRPEEFDHYVHFSSAVMGLLFGVPCLVTLVCYGLMARRLYQPLPGSAQSSSR	240
Qy	241	LRSLRTIAVVLTVFAVCFVPFHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANSC	300
Db	241	LRSLRTIAVVLTVFAVCFVPFHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANSC	300
Qy	301	LDPVLYLLTGDKYRRQLRQLCGGGKQPRTAASSLALVSLPEDSSCRWAATPQDSSCSTP	360
Db	301	LDPVLYLLTGDKYRRQLRQLCGGGKQPRTAASSLALVSLPEDSSCRWAATPQDSSCSTP	360
Qy	361	RADRL	365
Db	361	RADRL	365

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NEWS	3	Jun 03	New e-mail delivery for search results now available
NEWS	4	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS	5	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
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NEWS	8	Sep 16	Experimental properties added to the REGISTRY file
NEWS	9	Sep 16	CA Section Thesaurus available in CAPLUS and CA
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NEWS	19	Jan 29	Simultaneous left and right truncation added to COMPENDEX, ENERGY, INSPEC
NEWS	20	Feb 13	CANCERLIT is no longer being updated
NEWS	21	Feb 24	METADEx enhancements
NEWS	22	Feb 24	PCTGEN now available on STN
NEWS	23	Feb 24	TEMA now available on STN
NEWS	24	Feb 26	NTIS now allows simultaneous left and right truncation
NEWS	25	Feb 26	PCTFULL now contains images
NEWS	26	Mar 04	SDI PACKAGE for monthly delivery of multifile SDI results
NEWS	27	Mar 19	APOLLIT offering free connect time in April 2003
NEWS	28	Mar 20	EVENTLINE will be removed from STN
NEWS	29	Mar 24	PATDPAFULL now available on STN
NEWS	30	Mar 24	Additional information for trade-named substances without structures available in REGISTRY
NEWS	31	Apr 11	Display formats in DGENE enhanced
NEWS	32	Apr 14	MEDLINE Reload
NEWS	33	Apr 17	Polymer searching in REGISTRY enhanced
NEWS	34	Apr 21	Indexing from 1947 to 1956 being added to records in CA/CAPLUS
NEWS	35	Apr 21	New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX
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L3 24 PIROTTON SABINE

=> s parmentier marc /au

L4 282 PARMENTIER MARC

=> s boeynaems jean-marie /au

L5 122 BOEYNAEMS JEAN-MARIE

=> s (purinergic (a) receptor) (s) uridine

L6 85 (PURINERGIC (A) RECEPTOR) (S) URIDINE

=> s (purinergic (a) receptor) (s) uridine (s) protein

L7 20 (PURINERGIC (A) RECEPTOR) (S) URIDINE (S) PROTEIN

=> dup rem l7

PROCESSING COMPLETED FOR L7

L8 10 DUP REM L7 (10 DUPLICATES REMOVED)

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L8 ANSWER 1 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE

ACCESSION NUMBER: 2001:267356 BIOSIS  
DOCUMENT NUMBER: PREV200100267356  
TITLE: Effects of purine and pyrimidine nucleotides on intracellular Ca<sup>2+</sup> in human eosinophils: Activation of purinergic P2Y receptors.  
AUTHOR(S): Mohanty, Joy G. (1); Raible, Donald G.; McDermott, Lawrence J.; Pelleg, Amir; Schulman, Edward S.  
CORPORATE SOURCE: (1) Division of Pulmonary and Critical Care Medicine, MCP Hahnemann University, 245 N 15th St, Philadelphia, PA, 19102-1192 USA  
SOURCE: Journal of Allergy and Clinical Immunology, (May, 2001) Vol. 107, No. 5, pp. 849-855. print.  
ISSN: 0091-6749.  
DOCUMENT TYPE: Article  
LANGUAGE: English  
SUMMARY LANGUAGE: English

AB. . . human eosinophil intracellular Ca<sup>2+</sup> concentration; the mechanism of action is not fully known. ATP, a physiologic regulator, acts through 2 **purinergic receptor** types: cation channels (P2X) and G **protein**-coupled receptors (P2Y). Objective: This study is aimed at identifying the functional **purinergic receptors** in human eosinophils. Methods: The relative potency of ATP, **uridine** (UTP), cytidine (CTP), and inosine (ITP) 5'-triphosphates (P2Y agonists); 2-methylthio-ATP (P2Y1 agonist); and 2 P2X agonists, alpha,beta-methylene-ATP and beta,gamma-methylene-ATP on. . . the TH1 cytokine, IFN-gamma, expressed mRNA for P2X7, a receptor linked to apoptosis. Conclusions: These results suggest that the P2 **purinergic receptor** signal transduction pathways in eosinophils and neutrophils are different and are mediated by more than 1 subtype of functional P2Y. . .

L8 ANSWER 2 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
2

ACCESSION NUMBER: 2001:251017 BIOSIS  
DOCUMENT NUMBER: PREV200100251017  
TITLE: An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors.  
AUTHOR(S): Wittenberger, Timo (1); Schaller, H. Chica; Hellebrand, Susanne  
CORPORATE SOURCE: (1) Zentrum fuer Molekulare Neurobiologie, Martinistr. 52, 20246, Hamburg: wittenbe@uke.uni-hamburg.de Germany  
SOURCE: Journal of Molecular Biology, (30 March, 2001) Vol. 307, No. 3, pp. 799-813. print.  
ISSN: 0022-2836.  
DOCUMENT TYPE: Article  
LANGUAGE: English  
SUMMARY LANGUAGE: English

AB. . . developed a comprehensive expressed sequence tag database search method and used it for the identification of new members of the G-**protein** coupled receptor superfamily. Our approach proved to be especially useful for the detection of expressed sequence tag sequences that do not encode conserved parts of a **protein**, making it an ideal tool for the identification of members of divergent **protein** families or of **protein** parts without conserved domain structures in the expressed sequence tag database. At least 14 of the expressed sequence tags found with this strategy are promising candidates for new putative G-**protein** coupled receptors. Here, we describe the sequence and expression analysis of five new members of this receptor superfamily, namely GPR84,. . . the genomic structure and chromosomal localization of the respective genes applying in silico methods. A cluster of six closely related G-**protein** coupled receptors was found on the human chromosome 3q24-3q25. It consists of four orphan receptors (GPR86, GPR87, GPR91, and H963), the **purinergic receptor** P2Y1, and the **uridine** 5'-diphosphoglucose receptor KIAA0001. It

seems likely that these receptors evolved from a common ancestor and therefore might have related ligands.. . .

L8 ANSWER 3 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
3

ACCESSION NUMBER: 2001:381807 BIOSIS  
DOCUMENT NUMBER: PREV200100381807  
TITLE: Apical P2Y4 purinergic receptor controls K<sup>+</sup> secretion by vestibular dark cell epithelium.  
AUTHOR(S): Marcus, Daniel C. (1); Scofield, Margaret A.  
CORPORATE SOURCE: (1) Dept. of Anatomy and Physiology, Kansas State University, 1600 Denison Ave., Manhattan, KS, 66506: marcus@ksu.edu USA  
SOURCE: American Journal of Physiology, (July, 2001) Vol. 281, No. 1 Part 1, pp. C282-C289. print.  
ISSN: 0002-9513.  
DOCUMENT TYPE: Article  
LANGUAGE: English  
SUMMARY LANGUAGE: English

AB It was previously shown that K<sup>+</sup> secretion by vestibular dark cell epithelium is under control of G **protein**-coupled receptors of the P2Y family in the apical membrane that are activated by both purine and **uridine** nucleotides (P2Y2, P2Y4, or P2Y6). The present study was conducted to determine the subtype of **purinergic receptor** and to test whether these receptors undergo desensitization. The transepithelial short-circuit current represents electrogenic K<sup>+</sup> secretion and was found to. . .

L8 ANSWER 4 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
4

ACCESSION NUMBER: 2000:253886 BIOSIS  
DOCUMENT NUMBER: PREV200000253886  
TITLE: Phospholipase A2 and its products are involved in the purinergic receptor-mediated translocation of protein kinase C in CHO-K1 cells.  
AUTHOR(S): Shirai, Yasuhito; Kashiwagi, Kaori; Sakai, Norio; Saito, Naoaki (1)  
CORPORATE SOURCE: (1) Laboratory of Molecular Pharmacology, Biosignal Research Center, Kobe University, 1-1 Rokkodai-cho, Nada-ku, Kobe, 657-8501 Japan  
SOURCE: Journal of Cell Science, (April, 2000) Vol. 113, No. 8, pp. 1335-1343. print..  
ISSN: 0021-9533.  
DOCUMENT TYPE: Article  
LANGUAGE: English  
SUMMARY LANGUAGE: English

AB The signal transduction involved in the purinergic stimuli-induced activation of **protein** kinase C (PKC) in CHO-K1 cells was investigated. Purinergic stimuli such as adenosine triphosphate and **uridine** triphosphate induced a transient translocation of PKC epsilon, gamma, and delta from the cytoplasm to the plasma membrane. These translocations. . . the DAG antagonist and a phospholipase A2 (PLA2) inhibitor such as aristolochic acid, arachidonyltrifluoromethyl ketone, or bromoenol lactone inhibited the **purinergic receptor**-mediated translocation of PKC epsilon although each PLA2 inhibitor alone did not block the translocation. In contrast to the epsilon subtype, . .

L8 ANSWER 5 OF 10 MEDLINE DUPLICATE 5  
ACCESSION NUMBER: 1999054347 MEDLINE  
DOCUMENT NUMBER: 99054347 PubMed ID: 9840612  
TITLE: Expression of the P2Y6 purinergic receptor in human T cells infiltrating inflammatory bowel disease.  
AUTHOR: Somers G R; Hammet F M; Trute L; Southey M C; Venter D J

CORPORATE SOURCE: Department of Pathology, Peter MacCallum Cancer Institute,  
East Melbourne, Victoria, Australia.  
SOURCE: LABORATORY INVESTIGATION, (1998 Nov) 78 (11) 1375-83.  
Journal code: 0376617. ISSN: 0023-6837.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199812  
ENTRY DATE: Entered STN: 19990115  
Last Updated on STN: 19990115  
Entered Medline: 19981223

AB The human P2Y6 receptor is a member of the G-protein-coupled P2Y  
**purinergic receptor** family that responds to  
extracellular **uridine** diphosphate (UDP). In previous work, we  
cloned the human P2Y6 receptor from an activated T-cell library, and  
others have shown. . .

L8 ANSWER 6 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
6

ACCESSION NUMBER: 1998:358766 BIOSIS  
DOCUMENT NUMBER: PREV199800358766  
TITLE: Ca2+ dependent purinergic regulation of p42 and p44 MAP  
kinases in astroglial cultured cells.  
AUTHOR(S): Munsch, N.; Gavaret, J. M.; Pierre, M.  
CORPORATE SOURCE: Unite Recherhce Glande Thyroide, Regulation Hormonale, U96  
INSERM, 80 rue General Leclerc, 94276 Le Kremlin-Bicetre  
France  
SOURCE: Biomedicine & Pharmacotherapy, (May, 1998) Vol. 52, No. 4,  
pp. 180-186.  
ISSN: 0753-3322.  
DOCUMENT TYPE: Article  
LANGUAGE: English

AB. . . a signaling molecule for brain cells including astrocytes. In these  
cells, it has been shown that ATP stimulates myelin basic **protein**  
(MBP) kinase activity which is believed to represent the Erk family of MAP  
kinases. Indeed, we show that ATP activates. . . min. Effect of ATP is  
mimicked by 2-methylthio-ATP whereas alphabeta-methyleneadenosine 5'  
triphosphate (AMP-CPP) and adenosine do not promote any effect.  
**Uridine** triphosphate (UTP) activates also p42 and p44 MAP kinases.  
These observations indicate that p42-p44 MAP kinases activation can be  
obtained through P2y and P2u **receptors**. **Purinergic**  
stimulation of Erk is insensitive to pertussis toxin which inactivates  
heterotrimeric Gi **protein**. It is not inhibited by a PLA2  
inhibitor (4 bromophenacyl bromide (Bvariant phiB)) and the PI3 kinase  
inhibitor, wortmannin. In. . .

L8 ANSWER 7 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
7

ACCESSION NUMBER: 1997:353248 BIOSIS  
DOCUMENT NUMBER: PREV199799652451  
TITLE: Extracellular ATP promotes cellular growth of renal inner  
medullary collecting duct cells mediated via P-2u  
receptors.  
AUTHOR(S): Ishikawa, San-E (1); Higashiyama, Minori; Kusaka, Ikuyo;  
Saito, Takako; Nagasaka, Shoichiro; Fukuda, Shuichi; Saito,  
Toshikazu  
CORPORATE SOURCE: (1) Div. Endocrinol. and Metabolism, Dep. Med., Jichi Med.  
Sch., 3311-1 Yakushiji Minamikawachi-machi, Tochigi 329-04  
Japan  
SOURCE: Nephron, (1997) Vol. 76, No. 2, pp. 208-214.  
ISSN: 0028-2766.  
DOCUMENT TYPE: Article  
LANGUAGE: English



AB. . . calcium concentration - (Ca-2+)-i - in a dose-dependent manner. ATP also caused a transient cellular acidification. Extracellular ATP activated mitogen-activated **protein** (MAP) kinase and (3H)thymidine incorporation in a dose-dependent manner. However, such effects were not obtained with adenosine 5'-diphosphate, adenosine monophosphate, and adenosine. In addition, **uridine** triphosphate, a P-2u purinergic agonist, increased IP-3 production and activated MAP kinase. 2-Methylthio ATP, a P-2y purinergic agonist, also increased. . . renal inner medullary collecting duct cells. These results indicate that extracellular ATP activates phospholipase C mediated through P-2u and P-2, **purinergic receptors** and promotes cellular proliferation mediated through P-2u **purinergic receptors** in renal inner medullary collecting duct cells.

L8 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1996:29061 CAPLUS  
DOCUMENT NUMBER: 124:110212  
TITLE: Cloning and functional expression of a human uridine nucleotide receptor  
AUTHOR(S): Communi, Didier; Pirotton, Sabine; Parmentier, Marc; Boeynaems, Jean-Marie  
CORPORATE SOURCE: Institute of Interdisciplinary Res., Universite Libre de Bruxelles, Brussels, 1070, Belg.  
SOURCE: Journal of Biological Chemistry (1995), 270(52), 30849-52  
CODEN: JBCHA3; ISSN: 0021-9258  
PUBLISHER: American Society for Biochemistry and Molecular Biology  
DOCUMENT TYPE: Journal  
LANGUAGE: English  
IT **Receptors**  
RL: PRP (Properties)  
(**purinergic** P2Y, gene P2Y4, G **protein**-coupled; cloning and functional expression of human **uridine** nucleotide receptor)

L8 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1996:29060 CAPLUS  
DOCUMENT NUMBER: 124:108365  
TITLE: Cloning, expression, and chromosomal localization of the human uridine nucleotide receptor gene  
AUTHOR(S): Nguyen, Tuan; Erb, Laurie; Weisman, Gary A.; Marchese, Adriano; Heng, Henry H. Q.; Garrad, Richard C.; George, Susan R.; Turner, John T.; O'Dowd, Brian F.  
CORPORATE SOURCE: Addiction Research Foundation, Toronto, ON, M5S 2S1, Can.  
SOURCE: Journal of Biological Chemistry (1995), 270(52), 30845-48  
CODEN: JBCHA3; ISSN: 0021-9258  
PUBLISHER: American Society for Biochemistry and Molecular Biology  
DOCUMENT TYPE: Journal  
LANGUAGE: English  
IT **Receptors**  
RL: PRP (Properties)  
(**purinergic** P2Y, gene UNR, G **protein**-coupled; cloning, expression, and chromosomal localization of human **uridine** nucleotide receptor gene)

L8 ANSWER 10 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
8

ACCESSION NUMBER: 1994:266199 BIOSIS  
DOCUMENT NUMBER: PREV199497279199  
TITLE: External ATP and its analogs activate the cystic fibrosis

transmembrane conductance regulator by a cyclic  
AMP-independent mechanism.

AUTHOR(S): Cantiello, Horacio F. (1); Prat, Adriana G.; Reisin,  
Ignacio L.; Ercole, Liliana B.; Abraham, Edward H.; Amara,  
Jame F.; Gregory, Richard J.; Ausiello, Dennis A.  
CORPORATE SOURCE: (1) Renal Unit, Massachusetts Gen. Hosp. East, 149 13th  
St., Charlestown, MA 02129 USA  
SOURCE: Journal of Biological Chemistry, (1994) Vol. 269, No. 15,  
pp. 11224-11232.  
ISSN: 0021-9258.  
DOCUMENT TYPE: Article  
LANGUAGE: English

AB The cystic fibrosis transmembrane conductance regulator (CFTR) is a Cl-  
channel activated by **protein** kinase A and regulated by ATP in a  
complex manner. We have applied patch-clamp techniques to C127i mouse  
mammary carcinoma. . . . to activate non-rectifying, Cl--selective  
whole-cell currents in CFTR-transfected, but not mock-transfected cells.  
The ATP-mediated activation of CFTR was independent of **protein**  
kinase A since channel activation by ATP was preserved in cells that were  
(a) depleted of intracellular ATP, (b) incubated with the cAMP antagonist  
R-p-cAMPS, or (c) exposed to the **protein** kinase A inhibitor,  
5-24 amide. In each of these conditions, 8-Br-cAMP was no longer capable  
of activating CFTR. The possibility that the extracellular ATP activation  
of Cl- currents in CFTR-expressing C127i cells was mediated by a P-2-type  
**purinergic receptor** was supported by studies in which  
the effect of external ATP on the Cl- currents was mimicked by the ATP  
analogs, ATP-gamma-S and beta,gamma-methylene ATP, but not the  
**uridine** nucleotide, UTP. Single-channel analysis of ATP-activated  
Cl- currents under both cell-attached and excised, inside-out patch-clamp  
configurations indicated that this channel. . . . activated ATP currents  
in CFTR-transfected cells, a novel function of CFTR. These findings are  
consistent with the presence of a **purinergic receptor**  
signal transduction mechanism in C127i cells whose activation by external  
ATP is linked to the activation of CFTR in a. . . .

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1127.5	58.0	374	13	O57466	O57466 meleagris g
2	620.5	31.9	357	13	Q9DE05	Q9de05 raja erinac
3	608.5	31.3	361	13	Q90X57	Q90x57 xenopus lae
4	584	30.0	328	11	Q9ERK9	Q9erk9 mus musculu
5	514	26.4	337	4	Q96P68	Q96p68 homo sapien
6	422	21.7	399	11	Q8R3I1	Q8r3i1 mus musculu
7	403	20.7	372	4	Q9H1C0	Q9h1c0 homo sapien
8	379.5	19.5	384	13	Q98UH1	Q98uh1 brachydanio
9	378.5	19.5	330	4	Q9BXA5	Q9bxa5 homo sapien
10	378.5	19.5	334	4	Q8TDQ8	Q8tdq8 homo sapien
11	378.5	19.5	400	6	Q95M54	Q95m54 macaca fasc
12	378.5	19.5	454	4	Q9H573	Q9h573 homo sapien
13	373.5	19.2	377	13	Q98U14	Q98u14 brachydanio
14	371.5	19.1	390	11	Q8VI71	Q8vi71 mus musculu

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1944	100.0	365	1	P2Y4_HUMAN	P51582 homo sapien
2	1597	82.2	361	1	P2Y4_RAT	O35811 rattus norv
3	1561	80.3	361	1	P2Y4_MOUSE	Q9jjs7 mus musculu
4	1007.5	51.8	537	1	P2Y8_XENLA	P79928 xenopus lae
5	965	49.6	377	1	P2Y2_HUMAN	P41231 homo sapien
6	962.5	49.5	373	1	P2Y2_MOUSE	P35383 mus musculu
7	950	48.9	374	1	P2Y2_RAT	P41232 rattus norv
8	823	42.3	165	1	P2Y4_CRIGR	P58826 cricetulus
9	641.5	33.0	373	1	P2YR_HUMAN	P47900 homo sapien
10	631	32.5	362	1	P2YR_MELGA	P49652 meleagris g
11	628	32.3	362	1	P2YR_CHICK	P34996 gallus

## RESULT 1

## P2Y4\_HUMAN

ID P2Y4\_HUMAN STANDARD; PRT; 365 AA.

AC P51582;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE P2Y purinoceptor 4 (P2Y4) (Uridine nucleotide receptor) (UNR) (P2P).

GN P2RY4 OR NRU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96125055; PubMed=8537336;

RA Communi D., Pirotton S., Parmentier M., Boeynaems J.-M.;

RT "Cloning and functional expression of a human uridine nucleotide receptor.";

RL J. Biol. Chem. 270:30849-30852(1995).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=96125054; PubMed=8537335;

RA Nguyen T., Erb L., Weisman G.A., Marchese A., Heng H.H.Q.,

RA Garrad R.C., George S.R., Turner J.T., O'Dowd B.F.;

RT "Cloning, expression, and chromosomal localization of the human

RT uridine nucleotide receptor gene.";

RL J. Biol. Chem. 270:30845-30848(1995).

RN [3]

RP SEQUENCE FROM N.A.

APL-2005

(OLC)

RC TISSUE=Pancreas;  
RX MEDLINE=96197801; PubMed=8617367;  
RA Stam N.J., Klomp J., van der Heuvel M., Olijve W.;  
RT "Molecular cloning and characterization of a novel orphan receptor  
RT (P2P) expressed in human pancreas that shows high structural homology  
RT to the P2U purinoceptor.";  
RL FEBS Lett. 384:260-264(1996).  
CC -!- FUNCTION: Receptor for UTP and UDP coupled to G-proteins that  
CC activate a phosphatidylinositol-calcium second messenger system.  
CC Not activated by ATP or ADP.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Pancreas.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X91852; CAA62963.1; -.  
DR EMBL; U40223; AAC50347.1; -.  
DR EMBL; X96597; CAA65415.1; -.  
DR HSSP; P34996; 1DDD.  
DR Genew; HGNC:8542; P2RY4.  
DR MIM; 300038; -.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Polymorphism.  
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 35 61 1 (POTENTIAL).  
FT DOMAIN 62 72 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 73 95 2 (POTENTIAL).  
FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 113 131 3 (POTENTIAL).  
FT DOMAIN 132 154 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 155 174 4 (POTENTIAL).  
FT DOMAIN 175 196 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 197 222 5 (POTENTIAL).  
FT DOMAIN 223 246 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 247 269 6 (POTENTIAL).  
FT DOMAIN 270 287 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 288 309 7 (POTENTIAL).  
FT DOMAIN 310 365 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 108 185 BY SIMILARITY.  
FT VARIANT 168 168 V -> M (IN DBSNP:1152186).  
FT /FTId=VAR\_011854.  
FT VARIANT 178 178 N -> T (IN DBSNP:1152187).  
FT /FTId=VAR\_011855.  
FT VARIANT 191 191 P -> L (IN DBSNP:1152188).  
FT /FTId=VAR\_011856.  
FT CONFLICT 86 86 L -> V (IN REF. 2).  
FT CONFLICT 234 234 S -> A (IN REF. 2).  
SQ SEQUENCE 365 AA; 40963 MW; 23E0AFED3B7BDEED CRC64;

Query Match 100.0%; Score 1944; DB 1; Length 365;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKILLPVSYAVVFVLGLGLNAPTLWLF 60  
|  
Db 1 MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKILLPVSYAVVFVLGLGLNAPTLWLF 60  
  
Qy 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGEICKFVRFLFYWNLY 120  
|  
Db 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGEICKFVRFLFYWNLY 120

Qy 121 CSVLFLTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVWLVVAGCLVPNLFFVTTSNKG 180  
 |||||  
 Db 121 CSVLFLTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVWLVVAGCLVPNLFFVTTSNKG 180

Qy 181 TTVLCHDTRPEEFDHYVHFSSAVMGLLFGVPCLVTLVCYGLMARRLYQPLPGSAQSSSR 240  
 |||||  
 Db 181 TTVLCHDTRPEEFDHYVHFSSAVMGLLFGVPCLVTLVCYGLMARRLYQPLPGSAQSSSR 240

Qy 241 LRLSLRTIAVVLTVFAVCFVPPFHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANS 300  
 |||||  
 Db 241 LRLSLRTIAVVLTVFAVCFVPPFHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANS 300

Qy 301 LDPVLYLLTGDKYRRQLRQLCGGGKQPRTAASSLALVSLPEDSSCRWAATPQDSSCSTP 360  
 |||||  
 Db 301 LDPVLYLLTGDKYRRQLRQLCGGGKQPRTAASSLALVSLPEDSSCRWAATPQDSSCSTP 360

Qy 361 RADRL 365  
 |||||  
 Db 361 RADRL 365

# RESULT 2

## P2Y4\_RAT

ID P2Y4\_RAT STANDARD; PRT; 361 AA.  
 AC O35811;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE P2Y purinoceptor 4 (P2Y4).  
 GN P2RY4 OR P2Y4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RA Bogdanov Y.D., Wildman S., King B.F., Burntock G.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=98421785; PubMed=9751165;  
 RA Webb T.E., Henderson D., Roberts J.A., Barnard E.A.;  
 RT "Molecular cloning and characterization of the rat P2Y4 receptor.";  
 RL J. Neurochem. 71:1424-1434(1998).  
 CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that  
 CC activate a phosphatidylinositol-calcium second messenger system.  
 CC Not activated by ADP or UDP.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Widely expressed at low levels. In brain,  
 CC higher expression in the pineal gland and ventricular system.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; Y14705; CAA75007.1; -.  
 DR EMBL; Y11433; CAA72241.1; -.  
 DR HSSP; P34996; 1DDD.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

Query Match 82.2%; Score 1597; DB 1; Length 361;  
Best Local Similarity 82.7%; Pred. No. 2.9e-96;  
Matches 302; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

## SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1944	100.0	365	18	AAW23606	Human P2Y4 recepto
2	1944	100.0	365	22	AAE04391	Human P2Y4 pyrimid
3	1127.5	58.0	374	22	AAE04390	Turkey P2Y nucleot
4	1007.5	51.8	537	23	AAU74538	Human P2Y purinoce
5	965	49.6	377	22	AAE04392	Human P2-purinergi
6	965	49.6	377	22	AAE01143	Human purinergic r
7	965	49.6	377	22	AAE01144	Human purinergic r
8	962.5	49.5	373	23	AAE20604	Mus musculus GPCR
9	928	47.7	375	16	AAR72457	Human P20 receptor

10	641.5	33.0	373	22	AAE04389	Human P2-purinergi
11	641.5	33.0	373	23	AAU10983	Purinergic recepto
12	641.5	33.0	373	23	AAU10984	Purinergic recepto
13	634.5	32.6	373	23	AAU10985	Purinergic recepto
14	586	30.1	328	22	AAE04393	Human P2-purinergi
15	584	30.0	328	17	AAR91224	Mouse pancreas G-p
16	581	29.9	339	23	AAE18640	Human G-protein co
17	576	29.6	328	17	AAR91225	Human placenta G-p
18	571	29.4	328	18	AAW09433	Human placenta pur
19	516	26.5	259	21	AAB45375	Gene 37 human secr
20	514	26.4	337	22	AAU04375	Human G-protein co
21	514	26.4	337	23	AAO15399	

RESULT 1

AAW23606

ID AAW23606 standard; Protein; 365 AA.

XX

AC AAW23606;

XX

DT 31-MAR-1998 (first entry)

XX

DE Human P2Y4 receptor polypeptide.

XX

KW Receptor; P2Y4; pyrimidine binding; uridine triphosphate; UTP.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 35..61

FT /note= "membrane spanning domain I"

FT Domain 72..95

FT /note= "membrane spanning domain II"

FT Domain 113..131

FT /note= "membrane spanning domain III"

FT Domain 151..174

FT /note= "membrane spanning domain IV"

FT Domain 200..224

FT /note= "membrane spanning domain V"

FT Modified-site 238

FT /note= "potential protein kinase C  
(PKC) phosphorylation site"

FT Modified-site 243

FT /note= "potential calmodulin-dependent protein kinase  
and protein kinase C (PKC) phosphorylation site"

FT Domain 247..271

FT /note= "membrane spanning domain VI"

FT Modified-site 262

FT /note= "conserved His residue which is reported to  
play a role in the P2Y2 receptor activation  
by ATP and UTP"

FT Modified-site 265

FT /note= "conserved Arg residue which is reported to  
play a role in the P2Y2 receptor activation  
by ATP and UTP"

FT Modified-site 289

FT /note= "conserved Lys residue which is reported to  
play a role in the P2Y2 receptor activation  
by ATP and UTP"

FT Modified-site 292

FT /note= "conserved Arg residue which is reported to  
play a role in the P2Y2 receptor activation  
by ATP and UTP"

FT Domain 288..310

FT /note= "membrane spanning domain VII"

FT Modified-site 345

FT /note= "potential protein kinase C (PKC)  
phosphorylation site"

FT Modified-site 359

FT /note= "potential protein kinase C (PKC)  
phosphorylation site"

FT

XX  
 PN WO9719170-A1.  
 XX  
 PD 29-MAY-1997.  
 XX  
 PF 21-NOV-1996; 96WO-BE00123.  
 XX  
 PR 21-NOV-1995; 95EP-0870124.  
 XX  
 PA (EURO-) EUROSCREEN SA.  
 XX  
 PI Boeynaems J, Communi D, Parmentier M, Piroton S;  
 XX  
 DR WPI; 1997-402177/37.  
 DR N-PSDB; AAT74321.  
 XX  
 PT Receptor having preference for pyrimidine over purine nucleotide(s)  
 PT - especially uridine tri:phosphate, agonist and antagonists of which  
 PT are useful in treatment of cystic fibrosis  
 XX  
 PS Claim 1; Figure 1; 56pp; English.  
 XX  
 CC This sequence represents a novel human P2 receptor, P2Y4, which has a  
 CC preference for pyrimidine binding, especially uridine triphosphate.  
 CC This receptor could be used to screen for novel drugs which  
 CC specifically bind to it. Transgenic animals could be used to determine  
 CC the physiological effects of expressing varying levels of the receptor  
 CC or to identify novel agonists or antagonists. The agonists and  
 CC antagonists of human P2Y4 may be used, e.g., in treatment of cystic  
 CC fibrosis.  
 XX  
 SQ Sequence 365 AA;

Query Match 100.0%; Score 1944; DB 18; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-205;  
 Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKFIILLPVSYAVVFLVGLGLNAPTLWLF 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKFIILLPVSYAVVFLVGLGLNAPTLWLF 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGEICKFVRFLFYWNLY 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGEICKFVRFLFYWNLY 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 121 CSVLFLTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVWLVVAGCLVPNLFFVTTSNKG 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 CSVLFLTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVWLVVAGCLVPNLFFVTTSNKG 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 181 TTVLCHDTRPEEFDHYVHFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 TTVLCHDTRPEEFDHYVHFSSAVMGLLFGVPCLVTLVLCYGLMARRLYQPLPGSAQSSSR 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 241 LRSLRTIAVVLTVFAVCFVPFHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANSC 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 LRSLRTIAVVLTVFAVCFVPFHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANSC 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 301 LDPVLYLLTGDKYRRQLRQLCGGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 LDPVLYLLTGDKYRRQLRQLCGGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 361 RADRL 365  
 |||||  
 Db 361 RADRL 365

RESULT 2  
 AAE04391  
 ID AAE04391 standard; Protein; 365 AA.  
 XX  
 AC AAE04391;



XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human P2Y4 pyrimidinergic receptor.  
XX  
KW Human; P2-purinergeric receptor; P2Y1; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein; Gi; disseminated intravascular coagulation; P2Y4 pyrimidinergic receptor; thrombosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200146454-A1.  
XX  
PD 28-JUN-2001.  
XX  
PF 26-DEC-2000; 2000WO-US34998.  
XX  
PR 23-DEC-1999; 99US-0171622.  
XX  
PA (CORT-) COR THERAPEUTICS INC.  
XX  
PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ; Holoopeter G;  
PI  
XX  
DR WPI; 2001-418082/44.  
XX  
PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful  
PT for identifying binding partners and for diagnostic applications -  
XX  
PS Disclosure; Page 97-98; 108pp; English.  
XX  
CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed  
CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is  
CC the subtype of P2-purinergeric receptor. The P2Y12 receptor is expressed  
CC selectively in the platelets and brain, and couples to a pertussis toxin-  
CC sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor  
CC that responds to ADP. The invention also relates to a method for  
CC identifying an agent which is useful for modulating acute myocardial  
CC infarction, unstable angina, chronic stable angina, transient ischaemic  
CC attacks, strokes, peripheral vascular disease, preeclampsia, deep venous  
CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic  
CC thrombocytopaenic purpura or a bleeding disorder; thrombotic and  
CC restenotic complications following angioplasty, carotid endarterectomy,  
CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,  
CC stent placements or insertion of endovascular devices and prostheses.  
CC P2Y12 receptor is useful for identifying binding partners and for  
CC diagnostic applications. P2Y12 receptor provides targets for screening  
CC synthetic small molecules and combinatorial or naturally occurring  
CC compound libraries to regulate platelet aggregation, vascular injury, or  
CC disease as well as schizophrenia, eating disorders, depression, migraine  
CC and other brain disorders. The present sequence is human P2Y4  
CC pyrimidinergic receptor related to the invention.  
XX  
SQ Sequence 365 AA;

Query Match 100.0%; Score 1944; DB 22; Length 365;  
Best Local Similarity 100.0%; Pred. No. 1.4e-205;  
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKILLPVSYAVVFLVGLGLNAPTLLWLF 60  
Db 1 MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKILLPVSYAVVFLVGLGLNAPTLLWLF 60  
Qy 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGEICKFVRFLFYWNLY 120

Db 61 IFRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWPFGEICKFVRFLFYWNLY 120

Qy 121 CSVLFSLTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVWLVVAGCLVPNLFFVTTSNKG 180  
 |||||

Db 121 CSVLFSLTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVWLVVAGCLVPNLFFVTTSNKG 180

Qy 181 TTVLCHDTRPEEFDHYVHFSSAVMGLLFGVPCLVTLVCYGLMARRLYQPLPGSAQSSSR 240  
 |||||

Db 181 TTVLCHDTRPEEFDHYVHFSSAVMGLLFGVPCLVTLVCYGLMARRLYQPLPGSAQSSSR 240

Qy 241 LRSRLRTIAVVLTVFAVCFVPPHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANS 300  
 |||||

Db 241 LRSRLRTIAVVLTVFAVCFVPPHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANS 300

Qy 301 LDPVLYLLTGDKYRRLRQLCGGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360  
 |||||

Db 301 LDPVLYLLTGDKYRRLRQLCGGGKQPRTAASSLALVSLPEDSSCRWAATPDSSCSTP 360

Qy 361 RADRL 365  
 |||||

Db 361 RADRL 365

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	960.5	49.4	373	3	US-08-513-974B-373	Sequence 373, App
2	934	48.0	375	1	US-08-442-134A-2	Sequence 2, Appli
3	934	48.0	375	1	US-08-444-581B-2	Sequence 2, Appli
4	934	48.0	375	1	US-08-446-088A-2	Sequence 2, Appli
5	934	48.0	375	2	US-08-559-524A-3	Sequence 3, Appli
6	934	48.0	375	3	US-08-749-707-3	Sequence 3, Appli
7	621	31.9	373	2	US-08-559-524A-4	Sequence 4, Appli
8	621	31.9	373	3	US-08-749-707-4	Sequence 4, Appli
9	619	31.8	362	3	US-08-513-974B-374	Sequence 374, App
10	584.5	30.1	327	3	US-08-513-974B-372	Sequence 372, App

# ALIGNMENTS

## RESULT 1

US-08-513-974B-373

; Sequence 373, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji

; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo

; APPLICANT: Ohtaki, Tetsuya

; APPLICANT: Fukusumi, Shoji

; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF

; NUMBER OF SEQUENCES: 380

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:



Qy 260 PFHITRTIYYLARLLEADCRVLNIVNVVYKVTRPLASANSCLDPVLYLLTGDKYRRQLRQ 319  
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 Db 260 PFHVTRTLYYSFRLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAGQLRVRFARD 319

Qy 320 LCGGGKQPQ-----RTAASSLALVSLPEDSSCRWAATPQDS 355  
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SEQ ID NO: 1

#### SUMMARIES

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2	352	24.6	1842	1	US-08-444-581B-1	Sequence 1, Appli
3	352	24.6	1842	1	US-08-446-088A-1	Sequence 1, Appli
4	218.6	15.3	984	3	US-08-513-974B-57	Sequence 57, Appl
5	218.6	15.3	1023	3	US-08-513-974B-379	Sequence 379, App
6	210.8	14.8	984	3	US-08-513-974B-41	Sequence 41, Appl
7	210.8	14.8	1020	3	US-08-513-974B-370	Sequence 370, App
8	210.6	14.7	984	3	US-08-459-046-1	Sequence 1, Appli
9	128.4	9.0	1901	1	US-08-153-848-43	Sequence 43, Appl
10	128.4	9.0	1901	3	US-09-299-843A-43	Sequence 43, Appl
11	128.4	9.0	1901	4	US-09-088-337B-43	Sequence 43, Appl
12	128.4	9.0	1901	5	PCT-US93-11153-43	Sequence 43, Appl
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14	107.6	7.5	1679	1	US-08-202-056-6	Sequence 6, Appli
15	107.6	7.5	1679	1	US-08-076-093A-5	Sequence 5, Appli
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20	107.6	7.5	1679	2	US-08-801-238-5	Sequence 5, Appli
21	107.6	7.5	1679	2	US-08-801-228-5	Sequence 5, Appli
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23	107.6	7.5	1679	5	PCT-US94-06380-3	Sequence 3, Appli
24	107.6	7.5	2818	3	US-08-982-493-7	Sequence 7, Appli
25	107.6	7.5	2818	4	US-08-628-655-1	Sequence 1, Appli
26	104	7.3	1910	2	US-09-009-438-1	Sequence 1, Appli
27	104	7.3	1910	3	US-09-207-493-1	Sequence 1, Appli
28	98.6	6.9	1475	1	US-08-097-938-1	Sequence 1, Appli
29	98.6	6.9	1475	1	US-08-476-000-1	Sequence 1, Appli
30	98.6	6.9	1475	1	US-08-472-840-1	Sequence 1, Appli
31	98.6	6.9	1475	2	US-08-476-976-1	Sequence 1, Appli
32	98.6	6.9	1475	3	US-08-474-410-1	Sequence 1, Appli
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34	98.6	6.9	2732	1	US-08-476-000-60	Sequence 60, Appl
35	98.6	6.9	2732	1	US-08-472-840-60	Sequence 60, Appl
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#### SUMMARIES

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5	1365.2	95.5	1651	9	HSU40223	U40223 Human uridi
6	1230.4	86.1	1232	9	HSGPCRE	X96597 H.sapiens g
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8	808	56.5	215410	10	AC091784	AC091784 Genomic s
9	803.8	56.2	2684	10	RNP2Y4RG	Y14705 Rattus norv
10	796	55.7	1177	10	RNP2Y4REC	Y11433 R.norvegicu

11	784	54.9	1086	10	MMU277752	AJ277752 Mus muscu
12	416.4	29.1	1977	5	AF031897	AF031897 Meleagris
13	387.8	27.1	495	10	AF453823	AF453823 Cricetulu
14	380.8	26.6	2257	9	BC028135	BC028135 Homo sapi
15	380.8	26.6	2681	9	BC012104	BC012104 Homo sapi
16	380.8	26.6	123185	2	AP000587	AP000587 Homo sapi
17	379.2	26.5	2025	9	HSU07225	U07225 Homo sapien
18	379.2	26.5	196988	9	AP002761	AP002761 Homo sapi
19	359.2	25.1	1688	10	RNU56839	U56839 Rattus norv
20	359.2	25.1	2011	10	RATP2U	L46865 Rattus

# RESULT 1

A62985

LOCUS A62985 1429 bp DNA linear PAT 12-MAR-1998

DEFINITION Sequence 1 from Patent WO9719170.

ACCESSION A62985

VERSION A62985.1 GI:3716857

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1429)

AUTHORS Communi,D., Pirotton,S., Parmentier,M. and Boeynaems,J.

TITLE RECEPTOR AND NUCLEIC ACID MOLECULE ENCODING SAID RECEPTOR

JOURNAL Patent: WO 9719170-A 1 29-MAY-1997;

EUROSCREEN S A (BE)

FEATURES Location/Qualifiers

source

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CDS

181. .1278

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CYGLMARRLYQPLPGSAQSSSRLRLSLRTIAVVLTVFAVCFVFPFHITRTIYYLARLLEA  
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BASE COUNT 242 a 451 c 379 g 357 t

ORIGIN

Query Match 99.8%; Score 1425.8; DB 6; Length 1429;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	61	CTCCCTAGTGCTTCAACCACTGCTCTCCCTGCTCTACTTTTTTTGCTCCAGCTCAGGGAT	120
Db	61	CTCCCTAGTGCTTCAACCACTGCTCTCCCTGCTCTACTTTTTTTGCTCCAGCTCAGGGAT	120
Qy	121	GGGGGTGGGCAGGGAATCCTGCCACCCTCACTTCTCCCCTTCCCATCTCCAGGGGGGCC	180
Db	121	GGGGGTGGGCAGGGAATCCTGCCACCCTCACTTCTCCCCTTCCCATCTCCAGGGGGGCC	180
Qy	181	ATGGCCAGTACAGAGTCCTCCCTGTTGAGATCCCTAGGCCTCAGCCAGGTCTGGCAGC	240
Db	181	ATGGCCAGTACAGAGTCCTCCCTGTTGAGATCCCTAGGCCTCAGCCAGGTCTGGCAGC	240
Qy	241	AGTGAGGTGGAGCTGGACTGTTGGTTTGATGAGGATTCAAGTTCATCCTGCTGCCTGTG	300
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Qy	301	AGCTATGCAGTTGTCTTTGTGCTGGGCTTGGGCCTTAACGCCCCAACCCATATGGCTCTTC	360

Db	301		AGCTATGCAGTTGTCTTTGTGCTGGGCTTGGGCTTAACGCCCAACCCTATGGCTCTTC	360
Qy	361		ATCTTCCGCCTCCGACCTGGGATGCAACGGCCACCTACATGTTCCACCTGGCATTGTCA	420
Db	361		ATCTTCCGCCTCCGACCTGGGATGCAACGGCCACCTACATGTTCCACCTGGCATTGTCA	420
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Db	421		GACACCTTGTATGTGCTGTGCTGCGCTGCCCCACCCTCATCTACTATTATGCAGCCCAACCAC	480
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Db	661		TTGGTCGTAGCCGGCTGCCTCGTGCCCAACCTGTTCTTTGTGACAACCAGCAACAAAGGG	720
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Db	721		ACCACCGTCCTGTGCCATGACACCACTCGGCCTGAAGAGTTTGACCACTATGTGCACTTC	780
Qy	781		AGCTCGGCGTCAATGGGCTGCTCTTTGGCGTGCCCTGCCTGGTCACTCTTGTGCTAT	840
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RESULT 5

HSU40223

LOCUS HSU40223 1651 bp DNA linear PRI 19-JAN-1996

DEFINITION Human uridine nucleotide receptor (UNR) gene, complete cds.

ACCESSION U40223

VERSION U40223.1 GI:1117912

KEYWORDS G protein-coupled receptor; purinoceptor; PCR; intronless; UTP.

SOURCE Homo sapiens.

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1651)

AUTHORS Nguyen,T., Erb,L., Weisman,G.A., Marchese,A., Heng,H.H.,  
 Garrad,R.C., George,S.R., Turner,J.T. and O'Dowd,B.F.

TITLE Cloning, expression, and chromosomal localization of the human  
 uridine nucleotide receptor gene

JOURNAL J. Biol. Chem. 270 (52), 30845-30848 (1995)

MEDLINE 96125054

PUBMED 8537335

REFERENCE 2 (bases 1 to 1651)

AUTHORS O'Dowd,B.F., Nguyen,T., Marchese,A. and George,S.R.

TITLE Direct Submission

JOURNAL Submitted (07-NOV-1995) Brian F. O'Dowd, Department of  
 Pharmacology, University of Toronto, 8 Taddle Creek Road, Toronto,  
 Ontario M5S 1A8, Canada

FEATURES

source

Location/Qualifiers

1. .1651

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CDS

391. .1488

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BASE COUNT 290 a 522 c 429 g 410 t

ORIGIN

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 Best Local Similarity 98.4%; Pred. No. 0;  
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Db 211 AGGGAGGCTTGGGTAGGGGCCAGGCTAGCCTGAGTGCACCCAGATGCGCTTCTGT CAGCT 270

Qy 61 CTCCTAGTGCTTCAACCACTGCTCTCCCTGCTCTACTTTTTTTGCTCCAGCTCAGGGAT 120

Db 271 CTCCTAGTGCTTCAACCACTGCTCTCCCTGCTCTACTTTTTTTGCTCCAGCTCAGGGAT 330

Qy 121 GGGGGTGGGCAGGGAAATCCTGCCACCCTCACTTCTCCCTTCCCATCTCCAGGGGGGCC 180

Db 331 GGGGGTGGGCAGGGAATCCTGCCACCCTCACTTCTCCCTTCCCATCTCCAGGGGGGCC 390  
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 Db 571 ATCTTCCGCCTCCGACCCTGGGATGCAACGGCCACCTACATGTTCCACCTGGCATTGTCA 630  
 Qy 421 GACACCTGTATGTGCTGTGCTGCGCTGCCACCCTCATCTACTATTATGCAGCCCAACCAC 480  
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 Db 631 GACACCTGTATGTGCTGTGCTGCGCTGCCACCCTCATCTACTATTATGCAGCCCAACCAC 690  
 Qy 481 TGGCCCTTTGGCACTGAGATCTGCAAGTTCGTCGCTTTCTTTCTATTGGAACCTCTAC 540  
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 Db 691 TGGCCCTTTGGCACTGAGATCTGCAAGTTCGTCGCTTTCTTTCTATTGGAACCTCTAC 750  
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Db 1471 |||||AGGGCAGATAGATTGTAACACGGGAAGCCGGGAAGTGAGAGAAAAGGGGATGAGTGCAGG 1530
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Db 1531 |||||GCAGAGGTGAGGGAACCCAATAGTGATACCTGGTAAGGTGCTTCTTCCCTCTTTCCAG 1590
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Db 1591 |||||GGCTCTGGAGAGAAGCCCTCACCCCTGAGGTT 1622

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# RESULT 6

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LOCUS      HSGPCRE                      1232 bp    DNA        linear    PRI 11-JUN-1996
DEFINITION H.sapiens gene encoding G protein coupled receptor.
ACCESSION  X96597
VERSION    X96597.1  GI:1296631
KEYWORDS   G-protein coupled receptor.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1232)
AUTHORS    Stam,N.J., Klomp,J., Van de Heuvel,N. and Olijve,W.
TITLE      Molecular cloning and characterization of a novel orphan receptor
            (P2P) expressed in human pancreas that shows high structural
            homology to the P2U purinoceptor
JOURNAL     FEBS Lett. 384 (3), 260-264 (1996)
MEDLINE     96197801
PUBMED      8617367
REFERENCE  2 (bases 1 to 1232)
AUTHORS    Stam,N.J.
TITLE      Direct Submission
JOURNAL     Submitted (13-MAR-1996) N.J. Stam, NV. Organon, Department of
            Biotechnology and Biochemistry, P.O. Box 20, 5340 BH Oss,
            Netherlands
FEATURES
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            /translation="MASTESSLLRSLGLSPGPGSSEVELDCWFDEDFKFIILLPVSYAV
            VFVLGLGLNAPTLWLFI FRLRPWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWP
            FGTEICKFVRFLFYWNLYCSVLF LTCISVHRYLGICHPLRALRWGRPRLAGLLCLAVW
            LVVAGCLVPNLFVVTTSNKGTTVLCHDTRPEEFDHVVFSSAVMGLLFGVPCLVTLV
            CYGLMARRLYQPLPGSAQSSSRLRLRTIAVVLTVFVAVCFVPFHITRTIYYLARLLEA
            DCRVLNIWNVYKVT RPLASANSCLDPVLYLLTGDKYRRQLRQLCGGGKQPRTAASS
            LALVSLPEDSSCRWAATPQDSSCSTPRADRL"
BASE COUNT 204 a 397 c 319 g 312 t
ORIGIN

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Query Match      86.1%; Score 1230.4; DB 9; Length 1232;
Best Local Similarity 99.9%; Pred. No. 2.8e-295;
Matches 1231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 92 CTCTACTTTTTTTGCTCCAGCTCAGGGATGGGGGTGGGCAGGGAATCCTGCCACCCTCA 151
Db 1 CTCTACTTTTTTTGCTCCAGCTCAGGGATGGGGGTGGGCAGGGAATCCTGCCACCCTCA 60

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Qy	152	CTTCTCCCTTCCCATCTCCAGGGGGCCATGGCCAGTACAGAGTCCTCCCTGTTGAGAT	211
Db	61	CTTCTCCCTTCCCATCTCCAGGGGGCCATGGCCAGTACAGAGTCCTCCCTGTTGAGAT	120
Qy	212	CCCTAGGCCTCAGCCCAGGTCCTGGCAGCAGTGAGGTGGAGCTGGACTGTTGGTTTGATG	271
Db	121	CCCTAGGCCTCAGCCCAGGTCCTGGCAGCAGTGAGGTGGAGCTGGACTGTTGGTTTGATG	180
Qy	272	AGGATTTCAAGTTCATCCTGCTGCCTGTGAGCTATGCAGTTGTCTTTGTGCTGGGCTTGG	331
Db	181	AGGATTTCAAGTTCATCCTGCTGCCTGTGAGCTATGCAGTTGTCTTTGTGCTGGGCTTGG	240
Qy	332	GCCTTAACGCCCCAACCTATGGCTCTTCATCTTCCGCCTCCGACCTGGGATGCAACGG	391
Db	241	GCCTTAACGCCCCAACCTATGGCTCTTCATCTTCCGCCTCCGACCTGGGATGCAACGG	300
Qy	392	CCACCTACATGTTCCACCTGGCATTGTGAGACACCTTGTATGTGCTGTGCTGCCACCC	451
Db	301	CCACCTACATGTTCCACCTGGCATTGTGAGACACCTTGTATGTGCTGTGCTGCCACCC	360
Qy	452	TCATCTACTATTATGCAGCCCACAACCACTGGCCCTTGGCACTGAGATCTGCAAGTTCG	511
Db	361	TCATCTACTATTATGCAGCCCACAACCACTGGCCCTTGGCACTGAGATCTGCAAGTTCG	420
Qy	512	TCCGCTTTCTTTTCTATTGGAACCTCTACTGCAGTGTCTTTTCTCACCTGCATCAGCG	571
Db	421	TCCGCTTTCTTTTCTATTGGAACCTCTACTGCAGTGTCTTTTCTCACCTGCATCAGCG	480
Qy	572	TGCACCGCTACCTGGGCATCTGCCACCCACTTCGGGCACTACGCTGGGGCCGCCCTCGCC	631
Db	481	TGCACCGCTACCTGGGCATCTGCCACCCACTTCGGGCACTACGCTGGGGCCGCCCTCGCC	540
Qy	632	TCGCAGGCCTTCTCTGCCTGGCAGTTTGGTTGGTCGTAGCCGGCTGCCTCGTGCCCAACC	691
Db	541	TCGCAGGCCTTCTCTGCCTGGCAGTTTGGTTGGTCGTAGCCGGCTGCCTCGTGCCCAACC	600
Qy	692	TGTTCTTTGTGCAACCAAGCAACAAAGGGACCACCGTCTGTGCCATGACACCACTCGGC	751
Db	601	TGTTCTTTGTGCAACCAAGCAACAAAGGGACCACCGTCTGTGCCATGACACCACTCGGC	660
Qy	752	CTGAAGAGTTTGACCACTATGTGCACCTTCAGCTCGGCGGTATGGGGCTGCTCTTTGGCG	811
Db	661	CTGAAGAGTTTGACCACTATGTGCACCTTCAGCTCGGCGGTATGGGGCTGCTCTTTGGCG	720
Qy	812	TGCCCTGCCTGGTCACTCTTGTGTTGCTATGGACTCATGGCTCGTCGCCTGTATCAGCCCT	871
Db	721	TGCCCTGCCTGGTCACTCTTGTGTTGCTATGGACTCATGGCTCGTCGCCTGTATCAGCCCT	780
Qy	872	TGCCAGGCTCTGCACAGTCGTCTTCTCGCCTCCGCTCTCTCCGCACCATAGCTGTGGTGC	931
Db	781	TGCCAGGCTCTGCACAGTCGTCTTCTCGCCTCCGCTCTCTCCGCACCATAGCTGTGGTGC	840
Qy	932	TGACTGTCTTTGCTGTCTGCTTTCGTGCCTTTCCACATCACC CGCACCATTACTACCTGG	991
Db	841	TGACTGTCTTTGCTGTCTGCTTTCGTGCCTTTCCACATCACC CGCACCATTACTACCTGG	900
Qy	992	CCAGGCTGTTGGAAGCTGACTGCCGAGTACTGAACATTGTCAACGTGGTCTATAAAGTGA	1051
Db	901	CCAGGCTGTTGGAAGCTGACTGCCGAGTACTGAACATTGTCAACGTGGTCTATAAAGTGA	960
Qy	1052	CTCGGCCCCCTGGCCAGTGCCAACAGCTGCCTGGATCCTGTGCTCTACTTGCTCACTGGGG	1111
Db	961	CTCGGCCCCCTGGCCAGTGCCAACAGCTGCCTGGATCCTGTGCTCTACTTGCTCACTGGGG	1020
Qy	1112	ACAAATATCGACGTCAGCTCCGTCACTCTGTGGTGGTGGCAAGCCCCAGCCCCGACGG	1171
Db	1021	ACAAATATCGACGTCAGCTCCGTCACTCTGTGGTGGTGGCAAGCCCCAGCCCCGACGG	1080
Qy	1172	CTGCCTCTTCCCTGGCACTAGTGTCCCTGCCTGAGGATAGCAGCTGCAGGTGGGCGGCCA	1231

Db 1081 CTGCCTCTTCCCTGGCACTAGTGTCCCTGCGCTGAGGATAGCAGCTGCAGGTGGGCGGCCA 1140

Qy 1232 CCCCCCAGGACAGTAGCTGCTCTACTCCTAGGGCAGATAGATTGTAACACGGGAAGCCGG 1291  
 |||||

Db 1141 CCCCCCAGGACAGTAGCTGCTCTACTCCTAGGGCAGATAGATTGTAACACGGGAAGCCGG 1200

Qy 1292 CAAGTGAGAGAAAAGGGGATGAGTGCAGGGCA 1323  
 |||||

Db 1201 GAAGTGAGAGAAAAGGGGATGAGTGCAGGGCA 1232

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1425.8	99.8	1429	18	AAT74321	Human P2Y4 recepto
2	379.8	26.6	1163	22	AAD04981	Human purinergic r
3	379.2	26.5	2025	22	AAD04980	Human purinergic r
4	350.4	24.5	1842	16	AAQ88134	Human P20 receptor
5	343.4	24.0	2138	24	AAD32937	Mus musculus GPCR
6	343.4	24.0	2138	24	AAD32944	Mus musculus GPCR
7	218.6	15.3	984	17	AAT18368	Human placenta G-p
8	210.8	14.8	984	17	AAT18367	Mouse pancreas G-p
9	210.6	14.7	984	18	AAT70000	P2U purinergic rec
10	210.6	14.7	984	18	AAT47730	Human placenta pur
11	183	12.8	1076	24	AAD29667	Human G-protein co
12	180.2	12.6	1002	22	AAH73516	Human G protein-co
13	178.6	12.5	3143	24	AAS17746	Human genomic clon
14	171.2	12.0	1063	24	AAS98135	Human DNA for pote
15	154	10.8	850	24	AAS17747	Human P2Y-like G p
16	147.4	10.3	6721	24	AAS18599	Purinergic recepto
17	146.2	10.2	6721	24	AAS18600	Purinergic recepto
18	128.4	9.0	1020	21	AAA30601	Human G protein-co
19	128.4	9.0	1020	24	ABK52848	Human cysteinyl le
20	128.4	9.0	1901	15	AAQ66178	Seven transmembran
21	128.4	9.0	1901	19	AAV18356	Human R12 seven tr
22	128.4	9.0	1901	21	AAA91725	Human 7TM receptor
23	128.4	9.0	1901	24	ABK54254	Human 7 transmembr
24	128.4	9.0	2453	18	AAT44092	Human G-protein th
25	126.8	8.9	1020	21	AAA30718	DNA encoding human
26	123	8.6	1011	24	AAL43942	Human G protein-co
27	123	8.6	1014	22	AAS07948	Human cDNA encodin
28	123	8.6	1014	24	ABN85630	Human P2Y-like rec
29	123	8.6	1014	24	ABK11381	

## RESULT 1

AAT74321

ID AAT74321 standard; DNA; 1429 BP.

XX

AC AAT74321;

XX

DT 31-MAR-1998 (first entry)

XX

DE Human P2Y4 receptor genomic DNA.

XX

KW Receptor; P2Y4; pyrimidine binding; uridine triphosphate; UTP; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 181..1278

FT /\*tag= a

FT /product= P2Y4 receptor

XX

PN WO9719170-A1.

XX

PD 29-MAY-1997.

XX

XX

PR

PA

YY

FI  
VV

DR

DR  
VV

XX  
BFB

PT

PT

PS

XX

CC This sequence encodes a novel human P2 receptor, P2Y4, which has a  
CC preference for pyrimidine binding, especially uridine triphosphate.  
CC This receptor could be used to screen for novel drugs which  
CC specifically bind to it. Transgenic animals could be used to determine  
CC the physiological effects of expressing varying levels of the receptor  
CC or to identify novel agonists or antagonists. The agonists and  
CC antagonists of human P2Y4 may be used, e.g., in treatment of cystic  
CC fibrosis.

XX

Query Match 99.8%; Score 1425.8; DB 18; Length 1429;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	AAGGGAGCCTTGGGTAGGGGCCAGGCTAGCCTGAGTGCACCCAGATGCGCTTCTGT CAGCT	60
Db	1	AAGGGAGCCTTGGGTAGGGGCCAGGCTAGCCTGAGTGCACCCAGATGCGCTTCTGT CAGCT	60
Qy	61	CTCCCTAGTGCTTCAACCACTGCTCTCCCTGCTCTACTTTTTTTGCTCCAGCTCAGGGAT	120
Db	61	CTCCCTAGTGCTTCAACCACTGCTCTCCCTGCTCTACTTTTTTTGCTCCAGCTCAGGGAT	120
Qy	121	GGGGTGGGCAGGGAATCCTGCCACCCTCACTTCTCCCCTTCCCATCTCCAGGGGGGCC	180
Db	121	GGGGTGGGCAGGGAATCCTGCCACCCTCACTTCTCCCCTTCCCATCTCCAGGGGGGCC	180
Qy	181	ATGGCCAGTACAGAGTCTCCCTGTTGAGATCCCTAGGCCTCAGCCAGGTCTTGGCAGC	240
Db	181	ATGGCCAGTACAGAGTCTCCCTGTTGAGATCCCTAGGCCTCAGCCAGGTCTTGGCAGC	240
Qy	241	AGTGAGGTGGAGCTGGACTGTTGGTTTGATGAGGATTTCAAGTTCATCCTGCTGCCTGTG	300
Db	241	AGTGAGGTGGAGCTGGACTGTTGGTTTGATGAGGATTTCAAGTTCATCCTGCTGCCTGTG	300
Qy	301	AGCTATGCAGTTGTCTTTGTGCTGGGCTTGGGCCTTAACGCCCCAACCTATGGCTCTTC	360
Db	301	AGCTATGCAGTTGTCTTTGTGCTGGGCTTGGGCCTTAACGCCCCAACCTATGGCTCTTC	360
Qy	361	ATCTTCCGCCTCCGACCCTGGGATGCAACGGCCACCTACATGTTCCACCTGGCATTGTCA	420
Db	361	ATCTTCCGCCTCCGACCCTGGGATGCAACGGCCACCTACATGTTCCACCTGGCATTGTCA	420
Qy	421	GACACCTTGATGTGCTGTGCTGCTGCCACCCTCATCTACTATTATGCAGCCCAACAACAC	480
Db	421	GACACCTTGATGTGCTGTGCTGCTGCCACCCTCATCTACTATTATGCAGCCCAACAACAC	480
Qy	481	TGGCCCTTTGGCACTGAGATCTGCAAGTTCGTCCGCTTCTTTTCTATTGGAACCTCTAC	540
Db	481	TGGCCCTTTGGCACTGAGATCTGCAAGTTCGTCCGCTTCTTTTCTATTGGAACCTCTAC	540
Qy	541	TGCAGTGTCTTTTCTCCTCACCTGCATCAGCGTGCACCGCTACCTGGGCATCTGCCACCCA	600
Db	541	TGCAGTGTCTTTTCTCCTCACCTGCATCAGCGTGCACCGCTACCTGGGCATCTGCCACCCA	600

Qy 601 CTTCGGGCACTACGCTGGGGCCGCCCTCGCCTCGCAGGCCTTCTCTGCCTGGCAGTTTGG 660  
 |||||  
 Db 601 CTTCGGGCACTACGCTGGGGCCGCCCTCGCCTCGCAGGCCTTCTCTGCCTGGCAGTTTGG 660

Qy 661 TTGGTCGTAGCCGGCTGCCTCGTGCCCAACCTGTTCTTTGTGACAACCAGCAACAAAGGG 720  
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 Db 661 TTGGTCGTAGCCGGCTGCCTCGTGCCCAACCTGTTCTTTGTGACAACCAGCAACAAAGGG 720

Qy 721 ACCACCGTCCTGTGCCATGACACCACTCGGCCTGAAGAGTTTGACCACTATGTGCACTTC 780  
 |||||  
 Db 721 ACCACCGTCCTGTGCCATGACACCACTCGGCCTGAAGAGTTTGACCACTATGTGCACTTC 780

Qy 781 AGCTCGGCGGTATGGGGCTGCTCTTTGGCGTGCCCTGCCTGGTCACTCTTGTCTGCTAT 840  
 |||||  
 Db 781 AGCTCGGCGGTATGGGGCTGCTCTTTGGCGTGCCCTGCCTGGTCACTCTTGTCTGCTAT 840

Qy 841 GGACTCATGGCTCGTCGCCTGTATCAGCCCTTGCCAGGCTCTGCACAGTCGTCTTCTCGC 900  
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 Db 841 GGACTCATGGCTCGTCGCCTGTATCAGCCCTTGCCAGGCTCTGCACAGTCGTCTTCTCGC 900

Qy 901 CTCCGCTCTCTCCGCACCATAGCTGTGGTGCTGACTGTCTTGTCTGTCTGCTTCGTGCCT 960  
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 Db 901 CTCCGCTCTCTCCGCACCATAGCTGTGGTGCTGACTGTCTTGTCTGTCTGCTTCGTGCCT 960

Qy 961 TTCCACATCACCCGCACCATTTACTACCTGGCCAGGCTGTTGGAAGCTGACTGCCGAGTA 1020  
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 Db 961 TTCCACATCACCCGCACCATTTACTACCTGGCCAGGCTGTTGGAAGCTGACTGCCGAGTA 1020

Qy 1021 CTGAACATTGTCAACGTGGTCTATAAAGTGACTCGGCCCTGGCCAGTGCCAACAGCTGC 1080  
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 Db 1021 CTGAACATTGTCAACGTGGTCTATAAAGTGACTCGGCCCTGGCCAGTGCCAACAGCTGC 1080

Qy 1081 CTGGATCCTGTGCTCTACTTGCTCACTGGGGACAAATATCGACGTCAGCTCCGTGAGCTC 1140  
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 Db 1081 CTGGATCCTGTGCTCTACTTGCTCACTGGGGACAAATATCGACGTCAGCTCCGTGAGCTC 1140

Qy 1141 TGTGGTGGTGGCAAGCCCCAGCCCCGACGGCTGCCTCTTCCCTGGCACTAGTGTCCCTG 1200  
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 Db 1141 TGTGGTGGTGGCAAGCCCCAGCCCCGACGGCTGCCTCTTCCCTGGCACTAGTGTCCCTG 1200

Qy 1201 CCTGAGGATAGCAGCTGCAGGTGGGCGGCCACCCCCAGGACAGTAGCTGCTCTACTCCT 1260  
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 Db 1201 CCTGAGGATAGCAGCTGCAGGTGGGCGGCCACCCCCAGGACAGTAGCTGCTCTACTCCT 1260

Qy 1261 AGGGCAGATAGATTGTAACACGGGAAGCCGGGAAGTGAGAGAAAAGGGGATGAGTGCAGG 1320  
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 Db 1261 AGGGCAGATAGATTGTAACACGGGAAGCCGGGAAGTGAGAGAAAAGGGGATGAGTGCAGG 1320

Qy 1321 GCAGAGGTGAGGGAACCCAATAGTGATACCTGGTAAGGTGCTTCTTCTCTTTCCAGGC 1380  
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 Db 1321 GCAGAGGTGAGGGAACCCAATAGTGATACCTGGTAAGGTGCTTCTTCTCTTTCCAGGC 1380

Qy 1381 TCTGGAGAGAAGCCCTCACCCCTGAGGGTTGCCACGGAGGCAGGGATATC 1429  
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 Db 1381 TCTGGAGAGAAGCCCTCACCCCTGAGGGTTGCCACGGAGGCAGGGATATC 1429

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
c	1	345	24.1	2542	11 AK017378	AK017378 Mus muscu
	2	345	24.1	3001	11 AK005013	AK005013 Mus muscu
	3	232.2	16.2	1101	17 CNS0532S	AL318925 Tetraodon
	4	231.2	16.2	634	10 BB612642	BB612642 BB612642
	5	213	14.9	553	13 BM031311	BM031311 496677 MA
	6	210	14.7	613	9 AL657842	AL657842 AL657842
	7	203.6	14.2	638	9 AL675845	AL675845 AL675845
	8	202	14.1	641	14 BQ396255	BQ396255 NISC_ng19
	9	186.2	13.0	899	14 BQ959110	BQ959110 AGENCOURT